



1

SEQUENCE LISTING

<110> Valladeau, Jenny  
Ravel, Odile  
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Ford, John  
Lebecque, Serge J.E.  
Saeland, Sem

<120> Isolated Mammalian Membrane Protein Genes; Related Reagents

<130> SF0695 B

<140> US 09/862,802  
<141> 2001-05-22

<150> US 60/053,080  
<151> 1997-07-09

<150> US 09/111,470  
<151> 1998-07-08

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<170> PatentIn version 3.1

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ctccactagt tgagtgaag gaaggaggta atttaccacc atgtttgggt cctgtttata 180  
agatgtttta agaaagattt gaaacagatt ttctgaagaa agcagaagct ctcttcccat 240  
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Met Thr Ser Glu Ile Thr Tyr Ala Glu Val Arg Phe Lys Asn Glu Phe  
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Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg  
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Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala  
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Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala	
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Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr	
65 70 75 80	
aca aaa gag ctg gtt cat aca aca ttg gag tgt gtg aaa aaa aat atg	529
Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met	
85 90 95	
ccc gtg gaa gag aca gcc tgg agc tgt tgc cca aag aat tgg aag tca	577
Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser	
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Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln	
115 120 125	
gac agt gag aag gac tgt gct aga atg gag gct cac ctg ctg gtg ata	673
Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile	
130 135 140	
aac act caa gaa gag cag gat ttc atc ttc cag aat ctg caa gaa gaa	721
Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu	
145 150 155 160	
tct gct tat ttt gtg ggg ctc tca gat cca gaa ggt cag cga cat tgg	769
Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp	
165 170 175	
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Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His	
180 185 190	
cca cgt gag ccc agt gat ccc aat gag cgc tgc gtt gtg cta aat ttt	865
Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe	
195 200 205	
cgt aaa tca ccc aaa aga tgg ggc tgg aat gat gtt aat tgt ctt ggt	913
Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly	
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cct caa agg tca gtt tgt gag atg atg aag atc cac tta tgaactgaac	962
Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu	
225 230 235	
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Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg  
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Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala  
 35 40 45

Ser Leu Leu Ile Phe Phe Leu Leu Ala Ile Ser Phe Phe Ile Ala  
 50 55 60

Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr  
 65 70 75 80

Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met  
 85 90 95

Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser  
 100 105 110

Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln  
 115 120 125

Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile  
 130 135 140

Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu  
 145 150 155 160

Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp  
 165 170 175

Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His  
 180 185 190

Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe  
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Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly  
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<222> (608)..(673)
<223> short form lacks nucleotides 608-673
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<222> (775)..(776)
<223> ASGPRm (Table 2) has sequence insert encoding GEE between nucleot
ides 775-776
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<222> (1064)..(1064)
<223> nucleotide 1064 of DCMP2s may be A, which would encode Asn rather
      than Asp at the residue numbered 270
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caa aat tcc aaa ttt cag agg gac ctg gtg acc ctg aga aca gat ttt Gln Asn Ser Lys Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe 65 70 75	484
agc aac ttc acc tca aac act gtg gcg gag atc cag gca ctg act tcc Ser Asn Phe Thr Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser 80 85 90	532
cag ggc agc agc ttg gaa gaa acg ata gca tct ctg aaa gct gag gtg Gln Gly Ser Ser Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val 95 100 105	580
gag ggt ttc aag cag gaa cgg cag gca ggg gta tct gag ctc cag gaa Glu Gly Phe Lys Gln Glu Arg Gln Ala Gly Val Ser Glu Leu Gln Glu 110 115 120	628
cac act acg cag aag gca cac cta ggc cac tgt ccc cac tgc cca tct His Thr Thr Gln Lys Ala His Leu Gly His Cys Pro His Cys Pro Ser 125 130 135 140	676
gtg tgt gtc cca gtt cat tct gaa atg ctc ctg cga gtc cag cag ctg Val Cys Val Pro Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu 145 150 155	724
gtg caa gac ctg aag aaa ctg acc tgc cag gtg gct act ctc aac aac Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn 160 165 170	772
aat gcc tcc act gaa ggg acc tgc tgc ccc gtc aac tgg gtg gag cac Asn Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu His 175 180 185	820
caa gac agc tgc tac tgg ttc tct cac tct ggg atg tcc tgg gcc gag Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala Glu 190 195 200	868
gct gag aag tac tgc cag ctg aag aac gcc cac ctg gtg gtc atc aac Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile Asn 205 210 215 220	916
tcc agg gag gag cag aat ttt gtc cag aaa tat cta ggc tcc gca tac Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr 225 230 235	964
acc tgg atg ggc ctc agt gac cct gaa gga gcc tgg aag tgg gtg gat Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp 240 245 250	1012
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 Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr  
 285 290 295 300

cac tgg gtc tgc gag gct ggc ctg ggt cag acc agc cag gag agt cac 1204  
 His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser His  
 305 310 315

tgagctgcct ttggtgggac caccgggcca cagaaatggc ggtgggagga ggactcttct 1264

cacgacctcc tcgcaagacc gctctgggag agaaataagc actgggagat tggaagcact 1324

gctaacathtt tgaatttttt tctctttaat tttaaaaaga tggatatagt ttcttaagct 1384

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<222> (608)..(673)

<223> short form lacks nucleotides 608-673

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<222> (775)..(776)

<223> ASGPRm (Table 2) has sequence insert encoding GEE between nucleotides 775-776

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<223> nucleotide 1064 of DCMP2s may be A, which would encode Asn rather than Asp at the residue numbered 270

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Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys  
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Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln  
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Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly  
 35 40 45

Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys

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Phe 65	Gln 66	Arg 67	Asp 68	Leu 69	Val 70	Thr 71	Leu 72	Arg 73	Thr 74	Asp 75	Phe 76	Ser 77	Asn 78	Phe 79	Thr 80
Ser 81	Asn 82	Thr 83	Val 84	Ala 85	Glu 86	Ile 87	Gln 88	Ala 89	Leu 90	Thr 91	Ser 92	Gln 93	Gly 94	Ser 95	Ser 96
Leu 97	Glu 98	Glu 99	Thr 100	Ile 101	Ala 102	Ser 103	Leu 104	Lys 105	Ala 106	Glu 107	Val 108	Glu 109	Gly 110	Phe 111	Lys 112
Gln 113	Glu 114	Arg 115	Gln 116	Ala 117	Gly 118	Val 119	Ser 120	Glu 121	Leu 122	Gln 123	Glu 124	His 125	Thr 126	Thr 127	Gln 128
Lys 129	Ala 130	His 131	Leu 132	Gly 133	His 134	Cys 135	Pro 136	His 137	Cys 138	Pro 139	Ser 140	Val 141	Cys 142	Val 143	Pro 144
Val 145	His 146	Ser 147	Glu 148	Met 149	Leu 150	Leu 151	Arg 152	Val 153	Gln 154	Gln 155	Leu 156	Val 157	Gln 158	Asp 159	Leu 160
Lys 161	Lys 162	Leu 163	Thr 164	Cys 165	Gln 166	Val 167	Ala 168	Thr 169	Leu 170	Asn 171	Asn 172	Asn 173	Ala 174	Ser 175	Thr 176
Glu 177	Gly 178	Thr 179	Cys 180	Cys 181	Pro 182	Val 183	Asn 184	Trp 185	Val 186	Glu 187	His 188	Gln 189	Asp 190	Ser 191	Cys 192
Tyr 193	Trp 194	Phe 195	Ser 196	His 197	Ser 198	Gly 199	Met 200	Ser 201	Trp 202	Ala 203	Glu 204	Ala 205	Glu 206	Lys 207	Tyr 208
Cys 209	Gln 210	Leu 211	Lys 212	Asn 213	Ala 214	His 215	Leu 216	Val 217	Val 218	Ile 219	Asn 220	Ser 221	Arg 222	Glu 223	Glu 224
Gln 225	Asn 226	Phe 227	Val 228	Gln 229	Lys 230	Tyr 231	Leu 232	Gly 233	Ser 234	Ala 235	Tyr 236	Thr 237	Trp 238	Met 239	Gly 240
Leu 241	Ser 242	Asp 243	Pro 244	Glu 245	Gly 246	Ala 247	Trp 248	Lys 249	Trp 250	Val 251	Asp 252	Gly 253	Thr 254	Asp 255	Tyr 256
Ala 257	Thr 258	Gly 259	Phe 260	Gln 261	Asn 262	Trp 263	Lys 264	Pro 265	Gly 266	Gln 267	Pro 268	Asp 269	Asp 270	Trp 271	Gln 272
Gly 273	His 274	Gly 275	Leu 276	Gly 277	Gly 278	Gly 279	Glu 280	Asp 281	Cys 282	Ala 283	His 284	Phe 285	His 286	Pro 287	Asp 288
Gly 289	Arg 290	Trp 291	Asn 292	Asp 293	Asp 294	Val 295	Cys 296	Gln 297	Arg 298	Pro 299	Tyr 300	His 301	Trp 302	Val 303	Cys 304

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Gln Arg Leu Cys Ser Gly Pro Arg Leu Leu Leu Leu Ser Leu Gly Leu  
 35 40 45

Ser Leu Leu Leu Leu Val Val Val Cys Val Ile Gly Ser Gln Asn Ser  
 50 55 60

Gln Leu Gln Glu Glu Leu Arg Gly Leu Arg Glu Thr Phe Ser Asn Phe  
 65 70 75 80

Thr Ala Ser Thr Glu Ala Gln Val Lys Gly Leu Ser Thr Gln Gly Gly  
 85 90 95

Asn Val Gly Arg Lys Met Lys Ser Leu Glu Ser Gln Leu Glu Lys Gln  
 100 105 110

Gln Lys Asp Leu Ser Glu Asp His Ser Ser Leu Leu Leu His Val Lys  
 115 120 125

Gln Phe Val Ser Asp Leu Arg Ser Leu Ser Cys Gln Met Ala Ala Leu  
 130 135 140

Gln Gly Asn Gly Ser Glu Arg Thr Cys Cys Pro Val Asn Trp Val Glu  
 145 150 155 160

His Glu Arg Ser Cys Tyr Trp Phe Ser Arg Ser Gly Lys Ala Trp Ala  
 165 170 175



Asp Ala Asp Asn Tyr Cys Arg Leu Glu Asp Ala His Leu Val Val Val  
 180 185 190

Thr Ser Trp Glu Glu Gln Lys Phe Val Gln His His Ile Gly Pro Val  
 195 200 205

Asn Thr Trp Met Gly Leu His Asp Gln Asn Gly Pro Trp Lys Trp Val  
 210 215 220

Asp Gly Thr Asp Tyr Glu Thr Gly Phe Lys Asn Trp Arg Pro Glu Gln  
 225 230 235 240

Pro Asp Asp Trp Tyr Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala  
 245 250 255

His Phe Thr Asp Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro  
 260 265 270

Tyr Arg Trp Val Cys Glu Thr Glu Leu Asp Lys Ala Ser Gln Glu Pro  
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Pro Leu Leu  
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Arg Leu Cys Ser Met Val Cys Phe Ser Leu Leu Ala Leu Ser Phe Asn  
 35 40 45

Ile Leu Leu Leu Val Val Ile Cys Val Thr Gly Ser Gln Ser Ala Gln  
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Leu Gln Ala Glu Leu Arg Ser Leu Lys Glu Ala Phe Ser Asn Phe Ser



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<223> poly-A addition motif
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gaa gag cag gat ttc atc act ggg atc ttg gac act cat gct gct tat 776  
 Glu Glu Gln Asp Phe Ile Thr Gly Ile Leu Asp Thr His Ala Ala Tyr  
 155 160 165

ttt ata ggg ttg tgg gat aca ggc cat cgg caa tgg caa tgg gtt gat 824  
 Phe Ile Gly Leu Trp Asp Thr Gly His Arg Gln Trp Gln Trp Val Asp  
 170 175 180

cag aca cca tat gaa gaa agt atc aca ttc tgg cac aat ggt gag ccc 872  
 Gln Thr Pro Tyr Glu Glu Ser Ile Thr Phe Trp His Asn Gly Glu Pro  
 185 190 195

agc agt ggc aat gaa aaa tgt gct aca ata att tac cgt tgg aag act 920  
 Ser Ser Gly Asn Glu Lys Cys Ala Thr Ile Ile Tyr Arg Trp Lys Thr  
 200 205 210

gga tgg ggc tgg aac gat atc tct tgc agt ctt aaa cag aag tca gtt 968  
 Gly Trp Gly Trp Asn Asp Ile Ser Cys Ser Leu Lys Gln Lys Ser Val  
 215 220 225 230

tgt cag atg aag aaa ata aac tta tgaatcactc attcttcatg ggcattcgat 1022  
 Cys Gln Met Lys Lys Ile Asn Leu  
 235

tcattgttat ccaaccatta cacagacacc tgggaaattc tacagggttca cagaatttaa 1082

gtgggcagca aatgggttatg catacactgg cccacatata tccttgtgca tttaccacacc 1142

tactctgtca taaaatgaac tttcattgag aattttctat ataccacaga gtatacagag 1202

tcccttatgg acacacatgg aactttttgc catcttgttt actcatgcca ttgtatgata 1262

ggttctcttg acctatctgt ttctgtttct ctggtgtttt tttaatgtct ttggatttat 1322

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Pro Ile Arg Asp Leu Arg Lys Pro Gly Ser Pro Ser Leu Leu Leu Thr  
 35 40 45

Ser Leu Met Leu Leu Leu Leu Leu Leu Ala Ile Thr Phe Leu Val Ala  
 50 55 60

Phe Ile Ile Tyr Phe Gln Lys Tyr Ser Gln Leu Leu Glu Glu Lys Lys  
 65 70 75 80

Ala Ala Lys Asn Ile Met His Asn Glu Leu Asn Cys Thr Lys Ser Val  
 85 90 95

Ser Pro Met Glu Asp Lys Val Trp Ser Cys Cys Pro Lys Asp Trp Arg  
 100 105 110

Leu Phe Gly Ser His Cys Tyr Leu Val Pro Thr Val Ser Ser Ser Ala  
 115 120 125

Ser Trp Asn Lys Ser Glu Glu Asn Cys Ser Arg Met Gly Ala His Leu  
 130 135 140

Val Val Ile Gln Ser Gln Glu Glu Gln Asp Phe Ile Thr Gly Ile Leu  
 145 150 155 160

Asp Thr His Ala Ala Tyr Phe Ile Gly Leu Trp Asp Thr Gly His Arg  
 165 170 175

Gln Trp Gln Trp Val Asp Gln Thr Pro Tyr Glu Glu Ser Ile Thr Phe  
 180 185 190

Trp His Asn Gly Glu Pro Ser Ser Gly Asn Glu Lys Cys Ala Thr Ile  
 195 200 205

Ile Tyr Arg Trp Lys Thr Gly Trp Gly Trp Asn Asp Ile Ser Cys Ser  
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Leu Lys Gln Lys Ser Val Cys Gln Met Lys Lys Ile Asn Leu  
 225 230 235

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tgtgacaacc tcagagccgt gttggcccaa gc atg aca agg acg tat gaa aac 293  
Met Thr Arg Thr Tyr Glu Asn  
1 5  
ttc cag tac ttg gag aat aag gtg aaa gtc cag ggg ttt aaa aat ggg 341  
Phe Gln Tyr Leu Glu Asn Lys Val Lys Val Gln Gly Phe Lys Asn Gly  
10 15 20  
cca ctt cct ctc cag tcc ctc ctg ctg ctg gtc atc atc tgt gtg gtt 389  
Pro Leu Pro Leu Gln Ser Leu Leu Leu Leu Val Ile Ile Cys Val Val  
25 30 35  
gga ttc caa aat tcc aaa ttt cag agg gac ctg gtg acc ctg aga aca 437  
Gly Phe Gln Asn Ser Lys Phe Gln Arg Asp Leu Val Thr Leu Arg Thr  
40 45 50 55  
gat ttt agc aac ttc acc tca aac act gtg gcg gag atc cag gca ctg 485  
Asp Phe Ser Asn Phe Thr Ser Asn Thr Val Ala Glu Ile Gln Ala Leu  
60 65 70  
act tcc cag ggc agc agc ttg gaa gaa acg ata gca tct ctg aaa gct 533  
Thr Ser Gln Gly Ser Ser Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala  
75 80 85  
gag gtg gag ggt ttc aag cag gaa cgg cag gca gtt cat tct gaa atg 581  
Glu Val Glu Gly Phe Lys Gln Glu Arg Gln Ala Val His Ser Glu Met  
90 95 100  
ctc ctg cga gtc cag cag ctg gtg caa gac ctg aag aaa ctg acc tgc 629  
Leu Leu Arg Val Gln Gln Leu Val Gln Asp Leu Lys Lys Leu Thr Cys  
105 110 115  
cag gtg gct act ctc aac aac aat ggt gag gaa gcc tcc act gaa ggg 677  
Gln Val Ala Thr Leu Asn Asn Asn Gly Glu Glu Ala Ser Thr Glu Gly  
120 125 130 135  
acc tgc tgc ccc gtc aac tgg gtg gag cac caa gac agc tgc tac tgg 725  
Thr Cys Cys Pro Val Asn Trp Val Glu His Gln Asp Ser Cys Tyr Trp  
140 145 150

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Phe Ser His Ser Gly Met Ser Trp Ala Glu Ala Glu Lys Tyr Cys Gln	
155 160 165	
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Leu Lys Asn Ala His Leu Val Val Ile Asn Ser Arg Glu Glu Gln Asn	
170 175 180	
ttt gtc cag aaa tat cta ggc tcc gca tac acc tgg atg ggc ctc agt	869
Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr Thr Trp Met Gly Leu Ser	
185 190 195	
gac cct gaa gga gcc tgg aag tgg gtg gat gga aca gac tat gcg acc	917
Asp Pro Glu Gly Ala Trp Lys Trp Val Asp Gly Thr Asp Tyr Ala Thr	
200 205 210 215	
ggc ttc cag aac tgg aag cca ggc cag cca gac gac tgg cag ggg cac	965
Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro Asp Asp Trp Gln Gly His	
220 225 230	
ggg ctg ggt gga ggc gag gac tgt gct cac ttc cat cca gac ggc agg	1013
Gly Leu Gly Gly Gly Glu Asp Cys Ala His Phe His Pro Asp Gly Arg	
235 240 245	
tgg aat gac gac gtc tgc cag agg ccc tac cac tgg gtc tgc gag gct	1061
Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr His Trp Val Cys Glu Ala	
250 255 260	
ggc ctg ggt cag acc agc cag gag agt cac tgagctgcct ttggtgggac	1111
Gly Leu Gly Gln Thr Ser Gln Glu Ser His	
265 270	
cacccggcca cagaaatggc ggtgggagga ggactcttct cacgacctcc tcgcaagacc	1171
gctctgggag agaaataagc actgggagat tggaagcact gctaacattt tgaatttttt	1231
tctctttaat tttaaaaaga tggtatagtg ttcttaagct tttatttttt ttccaacttt	1291
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Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
1 5 10 15

Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Leu
20 25 30

Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys Phe Gln Arg  
 35 40 45

Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr Ser Asn Thr  
 50 55 60

Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser Leu Glu Glu  
 65 70 75 80

Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys Gln Glu Arg  
 85 90 95

Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu Val Gln  
 100 105 110

Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn Asn Gly  
 115 120 125

Glu Glu Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu  
 130 135 140

His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala  
 145 150 155 160

Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile  
 165 170 175

Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala  
 180 185 190

Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val  
 195 200 205

Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln  
 210 215 220

Pro Asp Asp Trp Gln Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala  
 225 230 235 240

His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro  
 245 250 255

Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser  
 260 265 270



His

<210> 11  
 <211> 75  
 <212> PRT  
 <213> Unknown

<220>  
 <223> mammalian protein

<400> 11

Glu Lys Met Ile Ile Lys Glu Leu Asn Tyr Thr Glu Leu Glu Cys Thr  
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Lys Trp Ala Ser Leu Leu Glu Asp Lys Val Trp Ser Cys Cys Pro Lys  
 20 25 30

Asp Trp Lys Pro Phe Gly Ser Tyr Cys Tyr Phe Thr Ser Thr Asp Leu  
 35 40 45

Val Ala Ser Trp Asn Glu Ser Lys Glu Asn Cys Phe His Met Gly Ala  
 50 55 60

His Leu Val Val Ile His Ser Gln Glu Glu Gln  
 65 70 75

<210> 12  
 <211> 292  
 <212> PRT  
 <213> Unknown

<220>  
 <223> mammalian protein (ASGPRm is a macrophage derived ASGPR)

<400> 12

Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys  
 1 5 10 15

Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln  
 20 25 30

Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly  
 35 40 45

Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys  
 50 55 60

Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr  
65 70 75 80

Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser  
85 90 95

Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys  
100 105 110

Gln Glu Arg Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln  
115 120 125

Leu Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn  
130 135 140

Asn Asn Gly Glu Glu Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn  
145 150 155 160

Trp Val Glu His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met  
165 170 175

Ser Trp Ala Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu  
180 185 190

Val Val Ile Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu  
195 200 205

Gly Ser Ala Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp  
210 215 220

Lys Trp Val Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys  
225 230 235 240

Pro Gly Gln Pro Asp Asp Trp Gln Gly His Gly Leu Gly Gly Gly Glu  
245 250 255

Asp Cys Ala His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys  
260 265 270

Gln Arg Pro Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser  
275 280 285

Gln Glu Ser His  
290

<210> 13  
 <211> 289  
 <212> PRT  
 <213> Unknown

<220>  
 <223> mammalian protein (DCMP2 short form)

<400> 13

Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys  
 1 5 10 15

Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln  
 20 25 30

Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly  
 35 40 45

Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys  
 50 55 60

Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr  
 65 70 75 80

Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser  
 85 90 95

Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys  
 100 105 110

Gln Glu Arg Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln  
 115 120 125

Leu Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn  
 130 135 140

Asn Asn Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu  
 145 150 155 160

His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala  
 165 170 175

Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile  
 180 185 190

Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala  
 195 200 205

Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val  
 210 215 220

Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln  
 225 230 235 240

Pro Asp Asn Trp Gln Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala  
 245 250 255

His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro  
 260 265 270

Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser  
 275 280 285

His